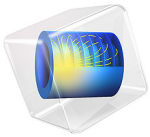

Glucose Sensor

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Introduction

Glucose sensing is one of the most widespread and commercially successful uses of electroanalysis. In an electrochemical glucose sensor, the concentration of glucose in a sample is measured using *amperometry*; that is, the measurement of an electric current. An applied voltage causes the oxidation of glucose, and the current due to this oxidation is measured at the electrode. In a well designed glucose sensor, there is a linear relationship between the glucose concentration and the current, enabling a calibrated measurement.

Typically, the oxidation of glucose does not occur directly at the working electrode where current is measured. Instead, the reaction is accomplished by a chemical oxidant and accelerated by a biological enzyme such as glucose oxidase (GOx), which makes the sensor specific to glucose and independent of the concentration of other oxidizable species that may be present in the analyte solution.

The reduced form of the oxidant, after its reaction with glucose, can be re-oxidized directly at the electrode. In nature, the oxidant is oxygen, but this suffers from slow kinetics and the rate of oxidation is perturbed by the oxygen concentration dissolved from atmosphere into the analyte solution.

Instead an inorganic oxidant with fast electrode kinetics, such as the hexacyanoferrate (III) anion (commonly, "ferricyanide"), is suitable for use in a glucose sensor, since the measured current is made independent of oxygen concentration and is not limited by slow electrode kinetics (Ref. 1).

This example demonstrates a steady-state analysis of the current drawn in a unit cell of solution above an interdigitated electrode, where the counter electrode reacts ferricyanide to ferrocyanide. The linearity of the response of the sensor is demonstrated for a typical range of glucose concentrations.

Model Definition

The model contains a single 2D domain representing a 100 μm-wide unit cell of solution above an interdigitated electrode (Figure 1). The real geometry is a periodic repetition of this unit cell in the x direction. The cell and electrode are assumed to extend sufficiently far out-of-plane of the model that the 2D approximation is suitable.

At the top of the unit cell is a bulk boundary where the concentrations are assumed to equal those in the bulk solution of the analyte. At the bottom of the unit cell, the $y = 0$ axis is divided by four points into separate electrode and insulator boundaries. The anode (working electrode) is at the center of the cell in the range $37.5\ \mu\text{m} < x < 62.5\ \mu\text{m}$. The

unit cell contains half of each of the two neighboring cathodes (counter electrodes) in the ranges $x < 12.5$ μm and $x > 87.5$ μm. Between the anode and cathode surfaces, a solid insulating material is present.

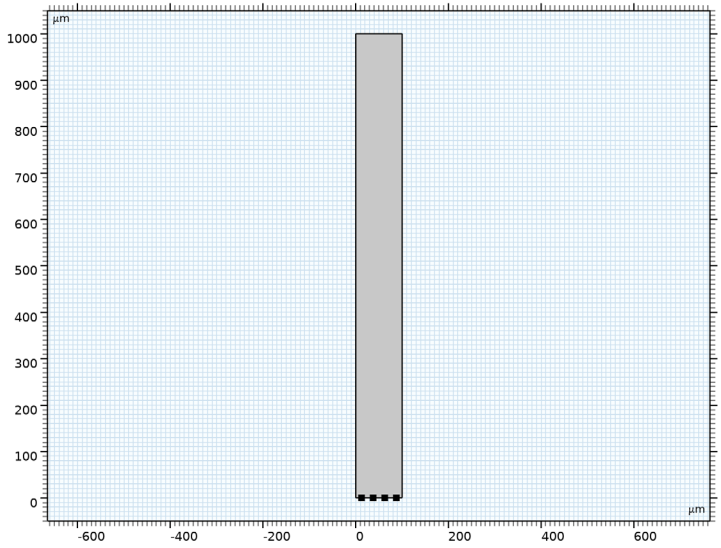


Figure 1: Model Geometry.

DOMAIN EQUATIONS

A large quantity of supporting electrolyte is present. This is inert salt added in electroanalytical experiments to increase the conductivity of the electrolyte without otherwise interfering with the reaction chemistry. Under these conditions, the resistance of the solution is sufficiently low that the electric field is negligible, and we can assume a constant electrolyte potential $\phi_l = 0$.

The Electroanalysis interface implements chemical species transport equations to describe the diffusion of the chemical species. The domain equation is the diffusion equation (also known as Fick's 2nd law). At steady-state, this reduces to:

$$\nabla \cdot (D_i \nabla c_i) = 0$$

for each species i. In this model three species are modeled: the active redox couple — ferricyanide and ferrocyanide anions — as well as the concentration of the glucose analyte

species. We ignore the products of the glucose oxidation since they do not affect the behavior of the sensor.

The enzyme-mediated reaction of the glucose with the ferricyanide anion occurs in the solution phase above the electrode:

$$\text{glucose} + \text{ferri} \leftrightarrow \text{products} + \text{ferro}$$

The rate of this reaction (mol/m^3) is given by a Michaelis–Menten rate law as (Ref. 2):

$$R = \frac{c_{\text{glucose}} V_{\max}}{(1 + K_{\text{m}} c_{\text{glucose}})}$$

Here, the parameter $V_{\max}$ is the maximum rate of the enzyme-catalyzed reaction, depending on the quantity of enzyme available, and the parameter K_{m} is a characteristic *Michaelis–Menten coefficient*. At large glucose concentration, the rate becomes independent of the glucose concentration and solely depends on the enzyme kinetics.

BOUNDARY EQUATIONS

At the bulk boundary (y = 1 mm), we assume a uniform concentration of each chemical species equal to its bulk concentration. The glucose concentration here is equivalent to that in the analyte mixture being measured; the ferricyanide:ferrocyanide ratio here is 50 000:1, with the ferricyanide anion present in bulk in a concentration of 50 mM. Because the analytical process is oxidizing with respect to the glucose analyte, more oxidant must be supplied.

At the insulating (inert) surfaces, the normal fluxes of all species are equal to zero, since this surface is impermeable and no species reacts there.

At the electrode boundaries, current is drawn from the interconversion of ferrocyanide and ferricyanide. By convention, electrochemical reactions are written in the reductive direction:

$$\text{ferri} + \text{e}^- \leftrightarrow \text{ferro}$$

The stoichiometric coefficient is –1 for ferricyanide, the "reactant" in the reductive direction, and +1 for ferrocyanide, the "product" in the reductive direction. This formulation is consistent at the anode also, although here the reaction proceeds favorably in the opposite, oxidative direction. The number of electrons transferred, n, equals one.

The current density for this reaction is given by the electroanalytical Butler–Volmer equation for an oxidation:

$$i_{\text{loc}} = nFk_0\left(c_{\text{ferro}}\exp\left(\frac{(n-\alpha_c)F\eta}{RT}\right) - c_{\text{ferri}}\exp\left(\frac{-\alpha_c F\eta}{RT}\right)\right)$$

in which k_0 is the *heterogeneous rate constant* of the reaction, α_c is the cathodic *transfer coefficient*, and η is the overpotential at the working electrode.

According to Faraday's laws of electrolysis, the flux of the reactant and product species are proportional to the current density drawn:

$$-\mathbf{n}\cdot\mathbf{J}_i = \frac{\nu_i i_{\text{loc}}}{nF}$$

This is expressed in the Electrode Surface boundary condition.

The total current recorded at the electrode can be extracted by integrating the local current density across the electrode surface. It is not sufficient to simply multiply by the area of the electrode, because the current density may be nonuniform. A nonlocal integration coupling is used to define an electrode current variable according to:

$$I_{\text{el}} = \int_S i_{\text{loc}}\,dA$$

where the integration is performed over the area of the working electrode.

The working electrode (anode) is held at +0.4 V versus the ferro/ferricyanide redox couple. The counter electrode is constrained to deliver an opposite current to the anode.

STATIONARY STUDY

This model calculates the steady-state current delivered under a constant applied potential. Therefore a Stationary study is chosen. A Parametric Sweep is used to compare the currents and concentration profiles for different external glucose concentrations in the analyte solution.

Results and Discussion

Figure 2 shows a typical concentration profile for the ferrocyanide ion in the unit cell. Ferrocyanide is generated in the solution between the electrodes and bulk by the enzyme-catalyzed oxidation of glucose. It reacts at the anode in the center of the unit cell to provide the working electrode current used to measure the concentration of glucose. Ferrocyanide is regenerated at the cathode counter electrodes at the left and right of the cell.

The diffusion of ferrocyanide from the counter to the working electrode is an example of a "redox cycling" process where a single redox reaction is driven in opposite directions at two electrodes with a small geometric separation. This cycling effect amplifies the current and so ensures a linear response to a wide range of glucose concentrations, as illustrated in Figure 3.

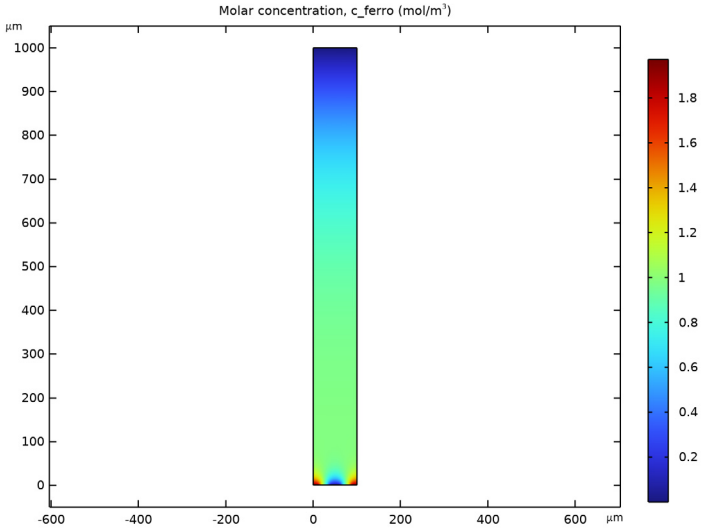


Figure 2: Ferrocyanide concentration for an external glucose concentration of 1 mol/m^3.

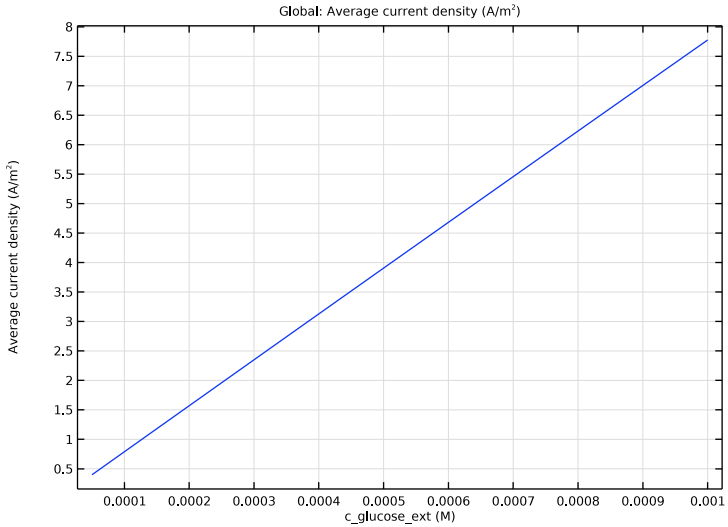


Figure 3: Current density versus glucose concentration.

References

1. J. Wang, "Electrochemical Glucose Biosensors," *Chem. Rev.*, vol. 108, no. 2, pp. 814–825, 2008.

2. P. Atkins and J. de Paula, *Physical Chemistry*, 9th ed., W. H. Freeman and Company, New York, 2010.

Application Library path: `Electrochemistry_Module/Electroanalysis/glucose_sensor`

Modeling Instructions

From the **File** menu, choose **New**.

NEW

In the **New** window, click **Model Wizard**.

MODEL WIZARD

1 In the **Model Wizard** window, Build the model in 2D with the Electroanalysis interface. Solve for three concentrations in a Stationary study.

2 click **2D**.

3 In the **Select Physics** tree, select **Electrochemistry** > **Electroanalysis (tcd)**.

4 Click **Add**.

5 In the **Number of species** text field, type 3.

6 In the **Concentrations (mol/m³)** table, enter the following settings:

c_glucose
c_ferro
c_ferri

7 Click **Study**.

8 In the **Select Study** tree, select **General Studies** > **Stationary**.

9 Click **Done**.

GEOMETRY 1

Set the length unit to micrometers and create the geometry using a rectangle and an array of points.

1 In the **Model Builder** window, under **Component 1 (comp1)** click **Geometry 1**.

2 In the **Settings** window for **Geometry**, locate the **Units** section.

3 From the **Length unit** list, choose **µm**.

Rectangle 1 (r1)

1 In the **Geometry** toolbar, click **Rectangle**.

2 In the **Settings** window for **Rectangle**, locate the **Size and Shape** section.

3 In the **Width** text field, type 100.

4 In the **Height** text field, type 1000.

Point 1 (pt1)

1 In the **Geometry** toolbar, click **Point**.

2 In the **Settings** window for **Point**, locate the **Point** section.

3 In the **x** text field, type 12.5.

Array 1 (arr1)

1 In the **Geometry** toolbar, click **Transforms** and choose **Array**.

2 Select the object **pt1** only.

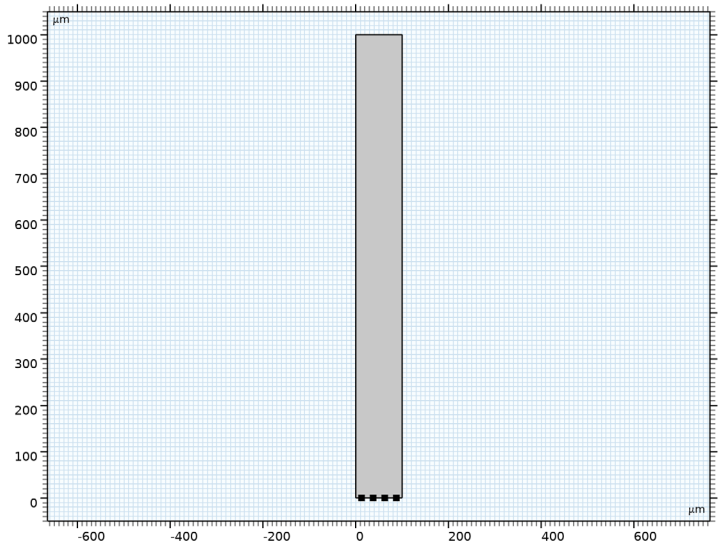
3 In the **Settings** window for **Array**, locate the **Size** section.

4 In the **x size** text field, type 4.

5 Locate the **Displacement** section. In the **x** text field, type 25.

6 Click **Build Selected**.

Your finished geometry should now look like this:



GLOBAL DEFINITIONS

Import the model parameters from a text file.

Parameters 1

1 In the **Model Builder** window, under **Global Definitions** click **Parameters 1**.

2 In the **Settings** window for **Parameters**, locate the **Parameters** section.

3 Click **Load from File**.

4 Browse to the model's Application Libraries folder and double-click the file `glucose_sensor_parameters.txt`.

DEFINITIONS

Add a nonlocal average coupling that will be used to calculate the average of the current density over one of the electrode surfaces.

Average 1 (aveop1)

1 In the **Definitions** toolbar, click **Nonlocal Couplings** and choose **Average**.

2 In the **Settings** window for **Average**, locate the **Source Selection** section.

3 From the **Geometric entity level** list, choose **Boundary**.

4 Select Boundary 5 only.

Variables 1

1 In the **Definitions** toolbar, click **Local Variables**.

2 In the **Settings** window for **Variables**, locate the **Variables** section.

3 In the table, enter the following settings:

Name	Expression	Unit	Description
R_MM	V_max*c_glucose/(Km+c_glucose)	mol/(m³·s)	Reaction rate of glucose
i_avg	aveop1(tcd.itot)		Average current density

The `i_avg` variable in marked in orange. This is because the `itot` variable has not yet been defined. It will be defined and added automatically to the model later on when you add the Electrode Surface feature.

ELECTROANALYSIS (TCD)

Now start defining the physics.

Electrode Surface 1

1 In the **Physics** toolbar, click **Boundaries** and choose **Electrode Surface**.

2 Select Boundary 5 only.

3 In the **Settings** window for **Electrode Surface**, locate the **Electrode Phase Potential Condition** section.

4 In the $\phi_{s,ext}$ text field, type `0.4`.

Electrode Reaction 1

1 In the **Model Builder** window, click **Electrode Reaction 1**.

2 In the **Settings** window for **Electrode Reaction**, locate the **Stoichiometric Coefficients** section.

3 In the ν_{cferro} text field, type `1`.

4 In the ν_{cferri} text field, type `-1`.

5 Locate the **Electrode Kinetics** section. In the $i_{0,ref}(T)$ text field, type `i0ref`.

Electrode Surface 2

1 In the **Physics** toolbar, click **Boundaries** and choose **Electrode Surface**.

2 Select Boundaries 2 and 7 only.

3 In the **Settings** window for **Electrode Surface**, locate the **Electrode Phase Potential Condition** section.

4 From the **Electrode phase potential condition** list, choose **Counter electrode**.

5 In the $\phi_{s,ext,init}$ text field, type `0.1`.

Electrode Reaction 1

1 In the **Model Builder** window, click **Electrode Reaction 1**.

2 In the **Settings** window for **Electrode Reaction**, locate the **Stoichiometric Coefficients** section.

3 In the ν_{cferro} text field, type `1`.

4 In the ν_{cferri} text field, type `-1`.

5 Locate the **Electrode Kinetics** section. In the $i_{0,ref}(T)$ text field, type `i0ref`.

Concentration 1

1 In the **Physics** toolbar, click **Boundaries** and choose **Concentration**.

2 Select Boundary 3 only.

3 In the **Settings** window for **Concentration**, locate the **Concentration** section.

4 Select the **Species c_glucose** checkbox.

5 In the $c_{0,cglucose}$ text field, type `c_glucose_ext`.

6 Select the **Species c_ferro** checkbox.

7 In the $c_{0,cferro}$ text field, type `c_ferro_ext`.

8 Select the **Species c_ferri** checkbox.

9 In the $c_{0,cferri}$ text field, type `c_ferri_ext`.

Reactions 1

1 In the **Physics** toolbar, click **Domains** and choose **Reactions**.

2 Select Domain 1 only.

3 In the **Settings** window for **Reactions**, locate the **Reaction Rates** section.

4 In the $R_{cglucose}$ text field, type `-R_MM`.

5 In the R_{cferro} text field, type `R_MM`.

6 In the R_{cferri} text field, type `-R_MM`.

Initial Values 1

1 In the **Model Builder** window, click **Initial Values 1**.

2 In the **Settings** window for **Initial Values**, locate the **Initial Values** section.

3 In the c_{glucose} text field, type `c_glucose_ext`.

4 In the c_{ferro} text field, type `c_ferro_ext`.

5 In the c_{ferri} text field, type `c_ferri_ext`.

MESH 1

The physics settings are now complete. Now customize the mesh and solve the problem.

1 In the **Model Builder** window, under **Component 1 (comp1)** right-click **Mesh 1** and choose **Edit Physics-Induced Sequence**.

Size

1 In the **Model Builder** window, under **Component 1 (comp1)** > **Mesh 1** click **Size**.

2 In the **Settings** window for **Size**, locate the **Element Size** section.

3 From the **Predefined** list, choose **Extra fine**.

Size 1

1 In the **Model Builder** window, right-click **Free Triangular 1** and choose **Size**.

2 In the **Settings** window for **Size**, locate the **Geometric Entity Selection** section.

3 From the **Geometric entity level** list, choose **Boundary**.

4 Select Boundaries 2 and 4–7 only.

5 Locate the **Element Size** section. From the **Predefined** list, choose **Extremely fine**.

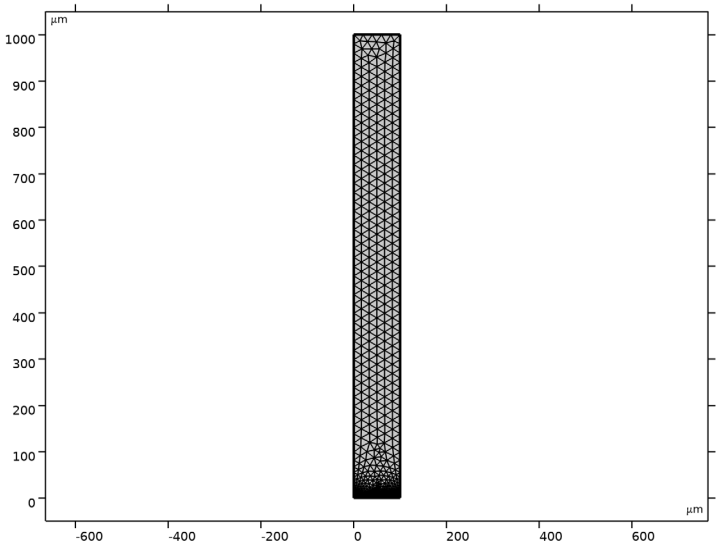
6 Click the **Custom** button.

7 Locate the **Element Size Parameters** section.

8 Select the **Maximum element size** checkbox. In the associated text field, type 1.

9 In the **Model Builder** window, right-click **Mesh 1** and choose **Build All**.

Your finished mesh should now look like this:



STUDY 1

Use an auxiliary sweep to solve for a range of different external concentration values for `c_glucose_ext`.

Step 1: Stationary

1 In the **Model Builder** window, under **Study 1** click **Step 1: Stationary**.

2 In the **Settings** window for **Stationary**, click to expand the **Study Extensions** section.

3 Select the **Auxiliary sweep** checkbox.

4 Click + **Add**.

5 In the table, enter the following settings:

Parameter name	Parameter value list	Parameter unit
c_glucose_ext (External glucose concentration)	`range(50,50,1000)`	`umol/L`

6 In the **Study** toolbar, click = **Compute**.

RESULTS

Concentration, ferro (tcd)

The second of the default concentration plots shows the ferro concentration.

Streamline 1

1 In the **Model Builder** window, expand the **Concentration, ferro (tcd)** node.

2 Right-click **Streamline 1** and choose **Disable**.

Concentration, ferro (tcd)

1 In the **Model Builder** window, click **Concentration, ferro (tcd)**.

2 In the **Settings** window for **2D Plot Group**, click to expand the **Title** section.

3 Find the **Solution** subsection. Clear the **Solution** checkbox.

4 Find the **Type and data** subsection. Clear the **Type** checkbox.

5 In the **Concentration, ferro (tcd)** toolbar, click **Plot**.

Average Current Density

Create a plot of the average current density for different `c_ferro_ext` values as follows:

1 In the **Results** toolbar, click **1D Plot Group**.

2 In the **Settings** window for **1D Plot Group**, type `Average Current Density` in the **Label** text field.

Global 1

1 Right-click **Average Current Density** and choose **Global**.

2 In the **Settings** window for **Global**, locate the **y-Axis Data** section.

3 In the table, enter the following settings:

Expression	Unit	Description
`i_avg`	`A/m^2`	`Average current density`

4 Click to expand the **Legends** section. Clear the **Show legends** checkbox.

5 In the **Average Current Density** toolbar, click **Plot**.